



74 5

SEQUENCE LISTING

<110> Messier, Walter

Sikela, James M

<120> Methods to Identify Polynucleotide and Polypeptide  
Sequences Which May Be Associated with Physiological  
and Medical Conditions

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<150> 09/591,435

<151> 2000-06-09

<150> 09/240,915

<151> 1999-01-29

<150> 60/073,263

<151> 1998-01-30

<150> 60/098,987

<151> 1998-09-02

<150> 09/942,252

<151> 2001-08-28

<160> 33

<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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<213> Pan troglodytes

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gtg cag gtg aca tgc agc acc tcc tgt gac cag ccc gac ttg ttg ggc 96

Val Gln Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Asp Leu Leu Gly

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ata gag acc ccg ttg cct aaa aag gag ttg ctt ctg ggt ggg aac aac 144

Ile Glu Thr Pro Leu Pro Lys Lys Glu Leu Leu Leu Gly Gly Asn Asn

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Trp Lys Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met	
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tgc tat tca aac tgc cct gat ggg cag tca aca gct aaa acc ttc ctc	240
Cys Tyr Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu	
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acc gtg tac tgg act cca gaa cgg gtg gaa ctg gca ccc ctc ccc tct	288
Thr Val Tyr Trp Thr Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser	
85 90 95	
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Trp Gln Pro Val Gly Lys Asp Leu Thr Leu Arg Cys Gln Val Glu Gly	
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Gly Ala Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys	
115 120 125	
gag ctg aaa cgg gag cca gct gtg ggg gag ccc gct gag gtc acg acc	432
Glu Leu Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr	
130 135 140	
acg gtg ctg gtg gag aga gat cac cat gga gcc aat ttc tcg tgc cgc	480
Thr Val Leu Val Glu Arg Asp His His Gly Ala Asn Phe Ser Cys Arg	
145 150 155 160	
act gaa ctg gac ctg cgg ccc caa ggg ctg cag ctg ttt gag aac acc	528

Thr Glu Leu Asp Leu Arg Pro Gln Gly Leu Gln Leu Phe Glu Asn Thr

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Ser Ala Pro His Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro

180

185

190

caa ctt gtc agc ccc cgg gtc cta gag gtg gac acg cag ggg acc gtg 624

Gln Leu Val Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val

195

200

205

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Val Cys Ser Leu Asp Gly Leu Phe Pro Val Ser Glu Ala Gln Val His

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ctg gca ctg ggg gac cag agg ttg aac ccc aca gtc acc tat ggc aat 720

Leu Ala Leu Gly Asp Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn

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gac tcc ttc tcg gcc aag gcc tca gtc agt gtg acc gca gag gac gag 768

Asp Ser Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu

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ggc acc cag cgg ctg acg tgt gca gta ata ctg ggg aac cag agc cgg 816

Gly Thr Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Arg

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265

270

gag aca ctg cag aca gtg acc atc tac agc ttt ccg gcg ccc aac gtg 864

Glu Thr Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val	
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Ile Leu Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys	
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tgt gag gcc cac cct aga gcc aag gtg acg ctg aat ggg gtt cca gcc	960
Cys Glu Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala	
305	310
315	320
cag cca gtg ggc ccg agg gtc cag ctc ctg ctg aag gcc acc cca gag	1008
Gln Pro Val Gly Pro Arg Val Gln Leu Leu Leu Lys Ala Thr Pro Glu	
325	330
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Asp Asn Gly Arg Ser Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly	
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Gln Leu Ile His Lys Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly	
355	360
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ccc cga ctg gac gag agg gat tgt ccg gga aac tgg acg tgg cca gaa	1152
Pro Arg Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu	
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aat tcc cag cag act cca atg tgc cag gct tcg ggg aac cca ttg ccc	1200
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Glu Leu Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Val Gly Glu				
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Ser Val Thr Val Thr Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala				
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Arg Ser Thr Gln Gly Glu Val Thr Arg Lys Val Thr Val Asn Val Leu				
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Ser Pro Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Ala Val				
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aag atc agg aaa tac aga cta caa cag gct caa aaa ggg acc ccc atg				1488
Lys Ile Arg Lys Tyr Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met				
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aaa ccg aac aca caa gcc acg cct ccc tga				1518
Lys Pro Asn Thr Gln Ala Thr Pro Pro				



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505

&lt;210&gt; 3

&lt;211&gt; 505

&lt;212&gt; PRT

&lt;213&gt; Pan troglodytes

&lt;400&gt; 3

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1

5

10

15

Val Gln Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Asp Leu Leu Gly

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25

30

Ile Glu Thr Pro Leu Pro Lys Lys Glu Leu Leu Leu Gly Gly Asn Asn

35

40

45

Trp Lys Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met

50

55

60

Cys Tyr Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu

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70

75

80

Thr Val Tyr Trp Thr Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser

85

90

95

Trp Gln Pro Val Gly Lys Asp Leu Thr Leu Arg Cys Gln Val Glu Gly

100

105

110



Gly Thr Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Arg

260

265

270

Glu Thr Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val

275

280

285

Ile Leu Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys

290

295

300

Cys Glu Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala

305

310

315

320

Gln Pro Val Gly Pro Arg Val Gln Leu Leu Leu Lys Ala Thr Pro Glu

325

330

335

Asp Asn Gly Arg Ser Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly

340

345

350

Gln Leu Ile His Lys Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly

355

360

365

Pro Arg Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu

370

375

380

Asn Ser Gln Gln Thr Pro Met Cys Gln Ala Ser Gly Asn Pro Leu Pro

385

390

395

400

Glu Leu Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Val Gly Glu

405

410

415

Ser Val Thr Val Thr Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala

420

425

430

Arg Ser Thr Gln Gly Glu Val Thr Arg Lys Val Thr Val Asn Val Leu

435

440

445

Ser Pro Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Ala Val

450

455

460

Ile Met Gly Thr Ala Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg

465

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caagccacgc ctccc 1515

<210> 5

<211> 1515

<212> DNA

<213> Pongo pygmaeus

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<211> 505

<212> PRT

<213> Homo sapiens



<400> 6

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Val Leu Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly

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30

Ile Glu Thr Pro Leu Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn

35

40

45

Arg Lys Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met

50

55

60

Cys Tyr Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu

65

70

75

80

Thr Val Tyr Trp Thr Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser

85

90

95

Trp Gln Pro Val Gly Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly

100

105

110

Gly Ala Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys

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120

125

Glu Leu Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr

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135

140

Thr Val Leu Val Arg Arg Asp His His Gly Ala Asn Phe Ser Cys Arg  
 145 150 155 160

Thr Glu Leu Asp Leu Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr  
 165 170 175

Ser Ala Pro Tyr Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro  
 180 185 190

Gln Leu Val Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val  
 195 200 205

Val Cys Ser Leu Asp Gly Leu Phe Pro Val Ser Glu Ala Gln Val His  
 210 215 220

Leu Ala Leu Gly Asp Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn  
 225 230 235 240

Asp Ser Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu  
 245 250 255

Gly Thr Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln  
 260 265 270

Glu Thr Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val  
 275 280 285

Ile Leu Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys

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Gln Pro Leu Gly Pro Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu			
	325	330	335
Asp Asn Gly Arg Ser Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly			
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Gln Leu Ile His Lys Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly			
	355	360	365
Pro Arg Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu			
	370	375	380
Asn Ser Gln Gln Thr Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro			
385	390	395	400
Glu Leu Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu			
	405	410	415
Ser Val Thr Val Thr Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala			
	420	425	430
Arg Ser Thr Gln Gly Glu Val Thr Arg Glu Val Thr Val Asn Val Leu			
	435	440	445

Ser Pro Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Ala Val  
450 455 460

Ile Met Gly Thr Ala Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg  
465 470 475 480

Lys Ile Lys Lys Tyr Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met  
485 490 495

Lys Pro Asn Thr Gln Ala Thr Pro Pro  
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<210> 7

<211> 254

<212> PRT

<213> Homo sapiens

<400> 7

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Gln Pro Glu Val Gly Gly Leu Glu Thr Ser Leu Asp Lys Ile Leu Leu  
35 40 45

Asp Glu Gln Ala Gln Trp Lys His Tyr Leu Val Ser Asn Ile Ser His  
 50 55 60

Asp Thr Val Leu Gln Cys His Phe Thr Cys Ser Gly Lys Gln Glu Ser  
 65 70 75 80

Met Asn Ser Asn Val Ser Val Tyr Gln Pro Pro Arg Gln Val Ile Leu  
 85 90 95

Thr Leu Gln Pro Thr Leu Val Ala Val Gly Lys Ser Phe Thr Ile Glu  
 100 105 110

Cys Arg Val Pro Thr Val Glu Pro Leu Asp Ser Leu Thr Leu Phe Leu  
 115 120 125

Phe Arg Gly Asn Glu Thr Leu His Tyr Glu Thr Phe Gly Lys Ala Ala  
 130 135 140

Pro Ala Pro Gln Glu Ala Thr Ala Thr Phe Asn Ser Thr Ala Asp Arg  
 145 150 155 160

Glu Asp Gly His Arg Asn Phe Ser Cys Leu Ala Val Leu Asp Leu Met  
 165 170 175

Ser Arg Gly Gly Asn Ile Phe His Lys His Ser Ala Pro Lys Met Leu  
 180 185 190

Glu Ile Tyr Glu Pro Val Ser Asp Ser Gln Met Val Ile Ile Val Thr  
 195 200 205

Val Val Ser Val Leu Leu Ser Leu Phe Val Thr Ser Val Leu Leu Cys  
210 215 220

Phe Ile Phe Gly Gln His Leu Arg Gln Gln Arg Met Gly Thr Tyr Gly  
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<212> PRT

<213> Homo sapiens

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Lys Ile Ala Leu Glu Thr Ser Leu Ser Lys Glu Leu Val Ala Ser Gly  
35 40 45

Met Gly Trp Ala Ala Phe Asn Leu Ser Asn Val Thr Gly Asn Ser Arg  
50 55 60

Ile Leu Cys Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser Ser  
65 70 75 80

Asn Ile Thr Val Tyr Gly Leu Pro Glu Arg Val Glu Leu Ala Pro Leu  
85 90 95

Pro Pro Trp Gln Pro Val Gly Gln Asn Phe Thr Leu Arg Cys Gln Val  
100 105 110

Glu Gly Gly Ser Pro Arg Thr Ser Leu Thr Val Val Leu Leu Arg Trp  
115 120 125

Glu Glu Glu Leu Ser Arg Gln Pro Ala Val Glu Glu Pro Ala Glu Val  
130 135 140

Thr Ala Thr Val Leu Ala Ser Arg Asp Asp His Gly Ala Pro Phe Ser  
145 150 155 160

Cys Arg Thr Glu Leu Asp Met Gln Pro Gln Gly Leu Gly Leu Phe Val  
165 170 175

Asn Thr Ser Ala Pro Arg Gln Leu Arg Thr Phe Val Leu Pro Val Thr  
180 185 190

Pro Pro Arg Leu Val Ala Pro Arg Phe Leu Glu Val Glu Thr Ser Trp  
195 200 205

Pro Val Asp Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala Gln

210	215	220	
Val Tyr Leu Ala Leu Gly Asp Gln Met Leu Asn Ala Thr Val Met Asn			
225	230	235	240
His Gly Asp Thr Leu Thr Ala Thr Ala Thr Ala Thr Ala Arg Ala Asp			
	245	250	255
Gln Glu Gly Ala Arg Glu Ile Val Cys Asn Val Thr Leu Gly Gly Glu			
	260	265	270
Arg Arg Glu Ala Arg Glu Asn Leu Thr Val Phe Ser Phe Leu Gly Pro			
	275	280	285
Ile Val Asn Leu Ser Glu Pro Thr Ala His Glu Gly Ser Thr Val Thr			
	290	295	300
Val Ser Cys Met Ala Gly Ala Arg Val Gln Val Thr Leu Asp Gly Val			
305	310	315	320
Pro Ala Ala Ala Pro Gly Gln Pro Ala Gln Leu Gln Leu Asn Ala Thr			
	325	330	335
Glu Ser Asp Asp Gly Arg Ser Phe Phe Cys Ser Ala Thr Leu Glu Val			
	340	345	350
Asp Gly Glu Phe Leu His Arg Asn Ser Ser Val Gln Leu Arg Val Leu			
	355	360	365



Tyr Gly Pro Lys Ile Asp Arg Ala Thr Cys Pro Gln His Leu Lys Trp  
370 375 380

Lys Asp Lys Thr Arg His Val Leu Gln Cys Gln Ala Arg Gly Asn Pro  
385 390 395 400

Tyr Pro Glu Leu Arg Cys Leu Lys Glu Gly Ser Ser Arg Glu Val Pro  
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Val Gly Ile Pro Phe Phe Val Asn Val Thr His Asn Gly Thr Tyr Gln  
420 425 430

Cys Gln Ala Ser Ser Ser Arg Gly Lys Tyr Thr Leu Val Val Val Met  
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Asp Ile Glu Ala Gly Ser Ser His Phe Val Pro Val Phe Val Ala Val  
450 455 460

Leu Leu Thr Leu Gly Val Val Thr Ile Val Leu Ala Leu Met Tyr Val  
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Phe Arg Glu His Gln Arg Ser Gly Ser Tyr His Val Arg Glu Glu Ser  
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Thr Tyr Leu Pro Leu Thr Ser Met Gln Pro Thr Glu Ala Met Gly Glu  
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Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe

35 40 45

Asn Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys

50 55 60

Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly

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Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Leu Glu His Cys Asn Phe  
35 40 45

Lys Asp Leu Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys  
50 55 60

Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly  
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Asn Glu Gln Leu Glu Asn Gly Gly Asn Glu Gln Leu Glu Asn Gly Gly

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Met Gln

1

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Phe Leu Glu Glu Val Gln Pro Tyr Arg Ala Leu Lys His Ser Asn Leu

5

10

15

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Leu Gln Cys Leu Ala Gln Cys Ala Glu Val Thr Pro Tyr Leu Leu Val

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25

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Met Glu Phe Cys Pro Leu Gly Asp Leu Lys Gly Tyr Leu Arg Ser Cys

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cgg gtg gcg gag tcc atg gct ccc gac ccc cgg acc ctg cag cgc atg 610



Arg Val Ala Glu Ser Met Ala Pro Asp Pro Arg Thr Leu Gln Arg Met

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Val His Ser Asp Leu Ala Leu Arg Asn Cys Leu Leu Thr Ala Asp Leu

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105

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Asp Tyr Phe Val Thr Ala Asp Gln Leu Trp Val Pro Leu Arg Trp Ile

115

120

125

130

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Ala Pro Glu Leu Val Asp Glu Val His Ser Asn Leu Leu Val Val Asp

135

140

145

cag acc aag agc ggg aat gtg tgg tcc ctg ggc gtg acc atc tgg gag 898

Gln Thr Lys Ser Gly Asn Val Trp Ser Leu Gly Val Thr Ile Trp Glu

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155

160

ctc ttt gag ctg ggc acg cag ccc tat ccc cag cac tcg gac cag cag 946

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cag ctg cag ctg acc ctg tcg gac cgc tgg tac gag gtg atg cag ttc 1042			
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Pro Gly Pro Gly Ala Ala Gly Pro Met Leu Gly Gly Val Val Glu Leu			
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Phe Pro Ala Thr Leu Ser Pro Gly Arg Thr Ala Arg Leu Gln Glu Leu				
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tgc gcc ccc gac ggc gcg ccc ccg ggc gtg gtt ccg gtg ctc agc gcg				1474
Cys Ala Pro Asp Gly Ala Pro Pro Gly Val Val Pro Val Leu Ser Ala				
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His Ser Pro Ser Leu Gly Ser Glu Tyr Phe Ile Arg Leu Glu Glu Ala				
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Ala Pro Ala Ala Gly His Asp Pro Asp Cys Ala Gly Cys Ala Pro Ser				
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Pro Pro Ala Thr Ala Asp Gln Asp Asp Asp Ser Asp Gly Ser Thr Ala				
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 Ala Ser Leu Ala Met Glu Pro Leu Leu Gly His Gly Pro Pro Val Asp

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 Val Pro Trp Gly Arg Gly Asp His Tyr Pro Arg Arg Ser Leu Ala Arg

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425

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gac ccg ctc tgc ccc tca cgc tct ccc tcg ccc tcg gcg ggg ccc ctg 1762  
 Asp Pro Leu Cys Pro Ser Arg Ser Pro Ser Pro Ser Ala Gly Pro Leu

435

440

445

450

agt ctg gcg gag gga gga gcg gag gat gca gac tgg ggc gtg gcc gcc 1810  
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455

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acc cca cgg gcc tcc ccc gag ccg ggg tac cct gga gag cct ctg ctt 2098  
Thr Pro Arg Ala Ser Pro Glu Pro Gly Tyr Pro Gly Glu Pro Leu Leu  
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Gly Leu Gln Ala Ala Ser Ala Gln Glu Pro Gly Cys Cys Pro Gly Leu  
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Pro His Leu Cys Ser Ala Gln Gly Leu Ala Pro Ala Pro Cys Leu Val  
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Thr Pro Ser Trp Thr Glu Thr Ala Ser Ser Gly Gly Asp His Pro Gln  
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Ala Glu Pro Lys Leu Ala Thr Glu Ala Glu Gly Thr Thr Gly Pro Arg  
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Leu Pro Leu Pro Ser Val Pro Ser Pro Ser Gln Glu Gly Ala Pro Leu	
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Pro Ser Glu Glu Ala Ser Ala Pro Asp Ala Pro Asp Ala Leu Pro Asp	
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Ser Pro Thr Pro Ala Thr Gly Gly Glu Val Ser Ala Ile Lys Leu Ala	
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Phe Arg Ser Leu Gln Lys Gln Val Gly Thr Pro Asp Ser Leu Asp Ser	
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ctg gac atc ccg tcc tca gcc agt gat ggt ggc tat gag gtc ttc agc	2674
Leu Asp Ile Pro Ser Ser Ala Ser Asp Gly Gly Tyr Glu Val Phe Ser	
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Pro Ser Ala Thr Gly Pro Ser Gly Gly Gln Pro Arg Ala Leu Asp Ser	
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ggc tat gac acc gag aac tat gag tcc cct gag ttt gtg ctc aag gag	2770
Gly Tyr Asp Thr Glu Asn Tyr Glu Ser Pro Glu Phe Val Leu Lys Glu	
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Ala Gln Glu Gly Cys Glu Pro Gln Ala Phe Ala Glu Leu Ala Ser Glu	
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Gly Glu Gly Pro Gly Pro Glu Thr Arg Leu Ser Thr Ser Leu Ser Gly	
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ctc aac gag aag aat ccc tac cga gac tct gcc tac ttc tca gac ctc	2914
Leu Asn Glu Lys Asn Pro Tyr Arg Asp Ser Ala Tyr Phe Ser Asp Leu	
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gag gct gag gcc gag gcc acc tca ggc cca gag aag aag tgc ggc ggg	2962
Glu Ala Glu Ala Glu Ala Thr Ser Gly Pro Glu Lys Lys Cys Gly Gly	
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gac cga gcc ccc ggg cca gag ctg ggc ctg ccg agc act ggg cag ccg	3010

Asp Arg Ala Pro Gly Pro Glu Leu Gly Leu Pro Ser Thr Gly Gln Pro

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860

865

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Ser Glu Gln Val Cys Leu Arg Pro Gly Val Ser Gly Glu Ala Gln Gly

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875

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tct ggc ccc ggg gag gtg ctg ccc cca ctg ctg cag ctt gaa ggg tcc 3106

Ser Gly Pro Gly Glu Val Leu Pro Pro Leu Leu Gln Leu Glu Gly Ser

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Gln Lys Arg Met Gly Gly Pro Gly Thr Pro Arg Ala Pro Leu Arg Leu

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1000

1005

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Tyr Ser Val Gln Glu Pro Ser Glu Asp Ser Glu Glu Glu Ala Pro Ala

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Val Pro Val Val Val Ala Glu Ser Gln Ser Ala Arg Asn Leu Arg Ser

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Leu Leu Lys Met Pro Ser Leu Leu Ser Glu Thr Phe Cys Glu Asp Leu

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gaa cgc aag aag aag gcc gtg tcc ttc ttc gac gac gtc acc gtc tac 3634

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Leu Phe Asp Gln Glu Ser Pro Thr Arg Glu Leu Gly Glu Pro Phe Pro

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Pro Ser Ala Pro Asn Arg Pro Gln Gln Ala Asp Gly Ser Pro Asn Gly				
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tcc aca gcg gaa gag ggt ggt ggg ttc gcg tgg gac gac gac ttc ccg				3826
Ser Thr Ala Glu Glu Gly Gly Gly Phe Ala Trp Asp Asp Asp Phe Pro				
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Leu Met Thr Ala Lys Ala Ala Phe Ala Met Ala Leu Asp Pro Ala Ala				
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Pro Ala Pro Ala Ala Pro Thr Pro Thr Pro Ala Pro Phe Ser Arg Phe				
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Thr Val Ser Pro Ala Pro Thr Ser Arg Phe Ser Ile Thr His Val Ser				
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gac tcg gac gcc gag tcc aag aga gga cct gaa gct ggt gcc ggg ggt				4018
Asp Ser Asp Ala Glu Ser Lys Arg Gly Pro Glu Ala Gly Ala Gly Gly				

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Glu Ser Lys Glu Ala

1205

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35 40 45

Ser Cys Arg Val Ala Glu Ser Met Ala Pro Asp Pro Arg Thr Leu Gln

50

55

60

Arg Met Ala Cys Glu Val Ala Cys Gly Val Leu His Leu His Arg Asn

65

70

75

80

Asn Phe Val His Ser Asp Leu Ala Leu Arg Asn Cys Leu Leu Thr Ala

85

90

95

Asp Leu Thr Val Lys Ile Gly Asp Tyr Gly Leu Ala His Cys Lys Tyr

100

105

110

Arg Glu Asp Tyr Phe Val Thr Ala Asp Gln Leu Trp Val Pro Leu Arg

115

120

125

Trp Ile Ala Pro Glu Leu Val Asp Glu Val His Ser Asn Leu Leu Val

130

135

140

Val Asp Gln Thr Lys Ser Gly Asn Val Trp Ser Leu Gly Val Thr Ile

145

150

155

160

Trp Glu Leu Phe Glu Leu Gly Thr Gln Pro Tyr Pro Gln His Ser Asp

165

170

175

Gln Gln Val Leu Ala Tyr Thr Val Arg Glu Gln Gln Leu Lys Leu Pro

180

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Lys Pro Gln Leu Gln Leu Thr Leu Ser Asp Arg Trp Tyr Glu Val Met

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His Leu Leu Leu Ser Tyr Leu Cys Ala Lys Gly Ala Thr Glu Ala Glu		
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Glu Glu Phe Glu Arg Arg Trp Arg Ser Leu Arg Pro Gly Gly Gly Gly		
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Val Gly Pro Gly Pro Gly Ala Ala Gly Pro Met Leu Gly Gly Val Val		
260	265	270
Glu Leu Ala Ala Ala Ser Ser Phe Pro Leu Leu Glu Gln Phe Ala Gly		
275	280	285
Asp Gly Phe His Ala Asp Gly Asp Asp Val Leu Thr Val Thr Glu Thr		
290	295	300
Ser Arg Gly Leu Asn Phe Glu Tyr Lys Trp Glu Ala Gly Arg Gly Ala		
305	310	315 320
Glu Ala Phe Pro Ala Thr Leu Ser Pro Gly Arg Thr Ala Arg Leu Gln		
325	330	335
Glu Leu Cys Ala Pro Asp Gly Ala Pro Pro Gly Val Val Pro Val Leu		
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Ser Ala His Ser Pro Ser Leu Gly Ser Glu Tyr Phe Ile Arg Leu Glu

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360

365

Glu Ala Ala Pro Ala Ala Gly His Asp Pro Asp Cys Ala Gly Cys Ala

370

375

380

Pro Ser Pro Pro Ala Thr Ala Asp Gln Asp Asp Asp Ser Asp Gly Ser

385

390

395

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Thr Ala Ala Ser Leu Ala Met Glu Pro Leu Leu Gly His Gly Pro Pro

405

410

415

Val Asp Val Pro Trp Gly Arg Gly Asp His Tyr Pro Arg Arg Ser Leu

420

425

430

Ala Arg Asp Pro Leu Cys Pro Ser Arg Ser Pro Ser Pro Ser Ala Gly

435

440

445

Pro Leu Ser Leu Ala Glu Gly Gly Ala Glu Asp Ala Asp Trp Gly Val

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Ala Ala Phe Cys Pro Ala Phe Phe Glu Asp Pro Leu Gly Thr Ser Pro

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Leu Gly Ser Ser Gly Ala Pro Pro Leu Pro Leu Thr Gly Glu Asp Glu

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495

Leu Glu Glu Val Gly Ala Arg Arg Ala Ala Gln Arg Gly His Trp Arg

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Trp Asp Pro Val Ser Ala Gly Cys His Ala Glu Gly Cys Pro Ser Pro		
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Leu Leu Gly Leu Gln Ala Ala Ser Ala Gln Glu Pro Gly Cys Cys Pro		
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Gly Leu Pro His Leu Cys Ser Ala Gln Gly Leu Ala Pro Ala Pro Cys		
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Leu Val Thr Pro Ser Trp Thr Glu Thr Ala Ser Ser Gly Gly Asp His		
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Pro Gln Ala Glu Pro Lys Leu Ala Thr Glu Ala Glu Gly Thr Thr Gly		
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Pro Arg Leu Pro Leu Pro Ser Val Pro Ser Pro Ser Gln Glu Gly Ala		
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Pro Leu Pro Ser Glu Glu Ala Ser Ala Pro Asp Ala Pro Asp Ala Leu		
645	650	655



Pro Asp Ser Pro Thr Pro Ala Thr Gly Gly Glu Val Ser Ala Ile Lys  
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Leu Ala Ser Ala Leu Asn Gly Ser Ser Ser Ser Pro Glu Val Glu Ala  
675 680 685

Pro Ser Ser Glu Asp Glu Asp Thr Ala Glu Ala Thr Ser Gly Ile Phe  
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Thr Asp Thr Ser Ser Asp Gly Leu Gln Ala Arg Arg Pro Asp Val Val  
705 710 715 720

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Asp Ser Leu Asp Ile Pro Ser Ser Ala Ser Asp Gly Gly Tyr Glu Val  
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Phe Ser Pro Ser Ala Thr Gly Pro Ser Gly Gly Gln Pro Arg Ala Leu  
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Pro Pro Glu Pro Gln Gly Pro Ala Lys Val Arg Pro Gly Pro Ser Pro		
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Ser Cys Ser Gln Phe Phe Leu Leu Thr Pro Val Pro Leu Arg Ser Glu		
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		960

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Asn Gly Ser Thr Ala Glu Glu Gly Gly Gly Phe Ala Trp Asp Asp Asp

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Phe Pro Leu Met Thr Ala Lys Ala Ala Phe Ala Met Ala Leu Asp Pro

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Arg Phe Thr Val Ser Pro Ala Pro Thr Ser Arg Phe Ser Ile Thr His

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cggccggagg aggaggagga ggacagttag gacagcgacg agtctgacga ggagctccgc 1260

tgctacagcg tccaggagcc tagcgaggac agcgaagagg aggcgccggc ggtgcccgtg 1320

gtggtggctg agagccagag cgcgcgcaac ctgcgcagcc tgctcaagat gccagcctg 1380



ctgtccgagg ccttctgcga ggacctggaa cgcaagaaga aggccgtgtc cttcttcgac 1440

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ccgggcgcca aggaatcgcc cccacgttc cttaggggga gccccggctc ttccagcgcc 1560

cccaaccggc cgcagcaggc tgatggctcc ccaaattggct ccacagcgga agaggggtgg 1620

gggttcgcgt gggacgacga cttcccgctg atgccggcca aggcagcctt cgccatggcc 1680

ctagaccggg cgcacccgc cccggtgcg cccacgcccg ctcccttctc gcgcttcacg 1740

gtgtcgcccg cgcccacgtc ccgcttctcc atcacgcacg tgtct 1785

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<211> 24

<212> DNA

<213> Pan troglodytes

<400> 19

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<210> 20

<211> 18

<212> DNA

<213> Homo sapiens

<400> 20

ggtgagggcc ccgggccc

18

<210> 21

<211> 18

<212> DNA

<213> Gorilla gorilla

<400> 21

ggcgagggcc ccgggccc

18

<210> 22

<211> 24

<212> DNA

<213> Pan troglodytes

<400> 22

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24

<210> 23

<211> 18

<212> DNA

<213> Homo sapiens

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cccacgcccg ctcccttc	18
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cccacgcccga cgcccgtcc cttc	24

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<211> 18

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cccacgcccg ctcccttc

18

<210> 28

<211> 24

<212> DNA

<213> Pan troglodytes

<400> 28

cccacgtcca cgtcccgtt ctcc

24

<210> 29

<211> 18

<212> DNA

<213> Homo sapiens

<400> 29

cccacgtccc gcttctcc

18

<210> 30

<211> 18

<212> DNA

<213> Gorilla gorilla

<400> 30

cccacgtccc gcttctcc

18

<210> 31

<211> 1335

<212> DNA

<213> Pan troglodytes

<400> 31

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cttgacagat gttgtaatca agggcctact ctaacagtga tttatagtga agatcatatt 180

attggagcat atgcagaaga ggggtaccag gmaagaaagt atgcttccat catccttttt 240

gcacttcaag agactaaaat ttcagaatgg aaactaggac tatatacacc agaaacactg 300

ttttgttgtg acgttgcaaa atataactcc ccaactaatt tccagataga tggaagaaat 360

agaaaagtga ttatggactt aaagacaatg gaaaatcttg gacttgctca aaattgtact 420

atctctattc aggattatga agtttttcga tgcgaagatt cactggacga aagaaagata 480  
 aaaggggtca ttgagctcag gaagagctta ctgtctgcct tgagaactta tgaaccatat 540  
 ggatccctgg ttcaacaaat acgaattctg ctgctgggtc caattggagc tgggaagtct 600  
 agctttttca actcagttag gtctgttttc caagggcatg taacgcatca ggctttggtg 660  
 ggactaata caactgggat atctgagaag tataggacat actctattag agacgggaaa 720  
 gatggcaaat acctgccatt tattctgtgt gactcactgg ggctgagtga gaaagaaggc 780  
 ggctgtgca tggatgacat atcctacatc ttgaacggtg acattcgtga tagataccag 840  
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 aaggacagaa ttcattgtgt ggcatttgta tttgatgcca gctctattga atacttctcc 960  
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 catgtggctt tgctcactca tgtggatagc atggatctga ttacaaaagg tgaccttata 1080  
 gaaatagaga gatgtgtgcc tgtgaggtcc aagctagagg aagtccaaag aaaacttgga 1140  
 tttgctcttt ctgacatctc ggtgggttagc aattattcct ctgagtggga gctggaccct 1200  
 gtaaaggatg ttctaattct ttctgctctg agacgaatgc tatgggctgc agatgacttc 1260

ttagaggatt tgccttttga gcaaataagg aatctaagg aggaaattat caactgtgca 1320

caaggaaaaa aatag

1335

<210> 32

<211> 1335

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)..(1332)

<220>

<223> M= A or C

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Met Ala Val Thr Thr Arg Leu Thr Trp Leu His Glu Lys Ile Leu Gln

1

5

10

15

aat cat ttt gga ggg aag cgg ctt agc ctt ctc tat aag ggt agt gtc 96

Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val

20

25

30

cat gga ttc cat aat gga gtt ttg ctt gac aga tgt tgt aat caa ggg 144

His Gly Phe His Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly

35

40

45

cct act cta aca gtg att tat agt gaa gat cat att att gga gca tat 192  
 Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr

50

55

60

gca gaa gag ggt tac cag gma aga aag tat gct tcc atc atc ctt ttt 240  
 Ala Glu Glu Gly Tyr Gln Xaa Arg Lys Tyr Ala Ser Ile Ile Leu Phe

65

70

75

80

gca ctt caa gag act aaa att tca gaa tgg aaa cta gga cta tat aca 288  
 Ala Leu Gln Glu Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Tyr Thr

85

90

95

cca gaa aca ctg ttt tgt tgt gac gtt gca aaa tat aac tcc cca act 336  
 Pro Glu Thr Leu Phe Cys Cys Asp Val Ala Lys Tyr Asn Ser Pro Thr

100

105

110

aat ttc cag ata gat gga aga aat aga aaa gtg att atg gac tta aag 384  
 Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys

115

120

125

aca atg gaa aat ctt gga ctt gct caa aat tgt act atc tct att cag 432  
 Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln

130

135

140

gat tat gaa gtt ttt cga tgc gaa gat tca ctg gac gaa aga aag ata 480  
 Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile

145

150

155

160



aaa ggg gtc att gag ctc agg aag agc tta ctg tct gcc ttg aga act 528  
 Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr

165 170 175

tat gaa cca tat gga tcc ctg gtt caa caa ata cga att ctg ctg ctg 576  
 Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu

180 185 190

ggt cca att gga gct ggg aag tct agc ttt ttc aac tca gtg agg tct 624  
 Gly Pro Ile Gly Ala Gly Lys Ser Ser Phe Phe Asn Ser Val Arg Ser

195 200 205

gtt ttc caa ggg cat gta acg cat cag gct ttg gtg ggc act aat aca 672  
 Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr

210 215 220

act ggg ata tct gag aag tat agg aca tac tct att aga gac ggg aaa 720  
 Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys

225 230 235 240

gat ggc aaa tac ctg cca ttt att ctg tgt gac tca ctg ggg ctg agt 768  
 Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser

245 250 255

gag aaa gaa ggc ggc ctg tgc atg gat gac ata tcc tac atc ttg aac 816  
 Glu Lys Glu Gly Gly Leu Cys Met Asp Asp Ile Ser Tyr Ile Leu Asn

260 265 270

ggt aac att cgt gat aga tac cag ttt aat ccc atg gaa tca atc aaa 864  
 Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys  
 275 280 285

tta aat cat cat gac tac att gat tcc cca tcg ctg aag gac aga att 912  
 Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile  
 290 295 300

cat tgt gtg gca ttt gta ttt gat gcc agc tct att gaa tac ttc tcc 960  
 His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Glu Tyr Phe Ser  
 305 310 315 320

tct cag atg ata gta aag atc aaa aga att cga agg gag ttg gta aac 1008  
 Ser Gln Met Ile Val Lys Ile Lys Arg Ile Arg Arg Glu Leu Val Asn  
 325 330 335

gct ggt gtg gta cat gtg gct ttg ctc act cat gtg gat agc atg gat 1056  
 Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp  
 340 345 350

ctg att aca aaa ggt gac ctt ata gaa ata gag aga tgt gtg cct gtg 1104  
 Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Val Pro Val  
 355 360 365

agg tcc aag cta gag gaa gtc caa aga aaa ctt gga ttt gct ctt tct 1152  
 Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser  
 370 375 380

gac atc tcg gtg gtt agc aat tat tcc tct gag tgg gag ctg gac cct 1200  
 Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro  
 385 390 395 400

gta aag gat gtt cta att ctt tct gct ctg aga cga atg cta tgg gct 1248  
 Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala  
 405 410 415

gca gat gac ttc tta gag gat ttg cct ttt gag caa ata ggg aat cta 1296  
 Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu  
 420 425 430

agg gag gaa att atc aac tgt gca caa gga aaa aaa tag 1335  
 Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys  
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<210> 33

<211> 444

<212> PRT

<213> Pan troglodytes

<220>

<223> M= A or C

<400> 33

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Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val

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His Gly Phe His Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly		
35	40	45
Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr		
50	55	60
Ala Glu Glu Gly Tyr Gln Xaa Arg Lys Tyr Ala Ser Ile Ile Leu Phe		
65	70	75
Ala Leu Gln Glu Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Tyr Thr		
85	90	95
Pro Glu Thr Leu Phe Cys Cys Asp Val Ala Lys Tyr Asn Ser Pro Thr		
100	105	110
Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys		
115	120	125
Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln		
130	135	140
Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile		
145	150	155
Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr		
165	170	175

Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu

180

185

190

Gly Pro Ile Gly Ala Gly Lys Ser Ser Phe Phe Asn Ser Val Arg Ser

195

200

205

Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr

210

215

220

Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys

225

230

235

240

Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser

245

250

255

Glu Lys Glu Gly Gly Leu Cys Met Asp Asp Ile Ser Tyr Ile Leu Asn

260

265

270

Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys

275

280

285

Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile

290

295

300

His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Glu Tyr Phe Ser

305

310

315

320

Ser Gln Met Ile Val Lys Ile Lys Arg Ile Arg Arg Glu Leu Val Asn

	325	330	335
Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp			
	340	345	350
Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Val Pro Val			
	355	360	365
Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser			
	370	375	380
Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro			
	385	390	395
			400
Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala			
	405	410	415
Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu			
	420	425	430
Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys			
	435	440	

<210> 34

<211> 1335

<212> DNA

<213> Homo sapiens

<400> 34

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cttgacagat gttgtaatca agggcctact ctaacagtga tttatagtga agatcatatt 180

attggagcat atgcagaaga gagttaccag gaaggaaagt atgcttccat catccttttt 240

gcacttcaag atactaaaat ttcagaatgg aaactaggac tatgtacacc agaaacactg 300

ttttgttgat atgttacaaa atataactcc ccaactaatt tccagataga tggaagaaat 360

agaaaagtga ttatggactt aaagacaatg gaaaatcttg gacttgctca aaattgtact 420

atctctattc aggattatga agtttttcga tgcgaagatt cactggatga aagaaagata 480

aaaggggtca ttgagctcag gaagagctta ctgtctgcct tgagaactta tgaaccatat 540

ggatccctgg ttcaacaaat acgaattctc ctctgggtc caattggagc tccaagtcc 600

agctttttca actcagtgag gtctgttttc caagggcatg taacgcatca ggctttgggtg 660

ggcactaata caactgggat atctgagaag tataggacat actctattag agacgggaaa 720

gatggcaaat acctgccgtt tattctgtgt gactcactgg ggctgagtga gaaagaaggc 780

ggcctgtgca gggatgacat attctatatc ttgaacggta acattcgtga tagataccag 840

tttaatccca tggaatcaat caaattaaat catcatgact acattgattc cccatcgctg 900  
 aaggacagaa ttcattgtgt ggcatttgta tttgatgcca gctctattca atacttctcc 960  
 tctcagatga tagtaaagat caaaagaatt caaagggagt tggtaaacgc tgggtgtgga 1020  
 catgtggctt tgctcactca tgtggatagc atggatttga ttacaaaagg tgaccttata 1080  
 gaaatagaga gatgtgagcc tgtgaggtcc aagctagagg aagtccaaag aaaacttgga 1140  
 tttgctcttt ctgacatctc ggtgggttagc aattattcct ctgagtggga gctggaccct 1200  
 gttaaaggatg ttctaattct ttctgctctg agacgaatgc tatgggctgc agatgacttc 1260  
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 caaggaaaaa aatag 1335

<210> 35

<211> 1335

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1335)



<400> 35

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Met Ala Val Thr Thr Arg Leu Thr Trp Leu His Glu Lys Ile Leu Gln

1 5 10 15

aat cat ttt gga ggg aag cgg ctt agc ctt ctc tat aag ggt agt gtc 96

Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val

20 25 30

cat gga ttc cgt aat gga gtt ttg ctt gac aga tgt tgt aat caa ggg 144

His Gly Phe Arg Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly

35 40 45

cct act cta aca gtg att tat agt gaa gat cat att att gga gca tat 192

Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr

50 55 60

gca gaa gag agt tac cag gaa gga aag tat gct tcc atc atc ctt ttt 240

Ala Glu Glu Ser Tyr Gln Glu Gly Lys Tyr Ala Ser Ile Ile Leu Phe

65 70 75 80

gca ctt caa gat act aaa att tca gaa tgg aaa cta gga cta tgt aca 288

Ala Leu Gln Asp Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Cys Thr

85 90 95

cca gaa aca ctg ttt tgt tgt gat gtt aca aaa tat aac tcc cca act 336

Pro Glu Thr Leu Phe Cys Cys Asp Val Thr Lys Tyr Asn Ser Pro Thr

100 105 110

aat ttc cag ata gat gga aga aat aga aaa gtg att atg gac tta aag 384  
 Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys

115

120

125

aca atg gaa aat ctt gga ctt gct caa aat tgt act atc tct att cag 432  
 Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln

130

135

140

gat tat gaa gtt ttt cga tgc gaa gat tca ctg gat gaa aga aag ata 480  
 Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile

145

150

155

160

aaa ggg gtc att gag ctc agg aag agc tta ctg tct gcc ttg aga act 528  
 Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr

165

170

175

tat gaa cca tat gga tcc ctg gtt caa caa ata cga att ctc ctc ctg 576  
 Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu

180

185

190

ggt cca att gga gct ccc aag tcc agc ttt ttc aac tca gtg agg tct 624  
 Gly Pro Ile Gly Ala Pro Lys Ser Ser Phe Phe Asn Ser Val Arg Ser

195

200

205

gtt ttc caa ggg cat gta acg cat cag gct ttg gtg ggc act aat aca 672  
 Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr

210

215

220

act ggg ata tct gag aag tat agg aca tac tct att aga gac ggg aaa	720
Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys	
225                                      230                                      235                                      240	
gat ggc aaa tac ctg ccg ttt att ctg tgt gac tca ctg ggg ctg agt	768
Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser	
245                                      250                                      255	
gag aaa gaa ggc ggc ctg tgc agg gat gac ata ttc tat atc ttg aac	816
Glu Lys Glu Gly Gly Leu Cys Arg Asp Asp Ile Phe Tyr Ile Leu Asn	
260                                      265                                      270	
ggt aac att cgt gat aga tac cag ttt aat ccc atg gaa tca atc aaa	864
Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys	
275                                      280                                      285	
tta aat cat cat gac tac att gat tcc cca tcg ctg aag gac aga att	912
Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile	
290                                      295                                      300	
cat tgt gtg gca ttt gta ttt gat gcc agc tct att caa tac ttc tcc	960
His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Gln Tyr Phe Ser	
305                                      310                                      315                                      320	
tct cag atg ata gta aag atc aaa aga att caa agg gag ttg gta aac	1008
Ser Gln Met Ile Val Lys Ile Lys Arg Ile Gln Arg Glu Leu Val Asn	
325                                      330                                      335	

gct ggt gtg gta cat gtg gct ttg ctc act cat gtg gat agc atg gat 1056

Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp

340

345

350

ttg att aca aaa ggt gac ctt ata gaa ata gag aga tgt gag cct gtg 1104

Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Glu Pro Val

355

360

365

agg tcc aag cta gag gaa gtc caa aga aaa ctt gga ttt gct ctt tct 1152

Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser

370

375

380

gac atc tcg gtg gtt agc aat tat tcc tct gag tgg gag ctg gac cct 1200

Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro

385

390

395

400

gta aag gat gtt cta att ctt tct gct ctg aga cga atg cta tgg gct 1248

Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala

405

410

415

gca gat gac ttc tta gag gat ttg cct ttt gag caa ata ggg aat cta 1296

Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu

420

425

430

agg gag gaa att atc aac tgt gca caa gga aaa aaa tag 1335

Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys

435

440

445

<210> 36

<211> 444

<212> PRT

<213> Homo sapiens

<400> 36

Met Ala Val Thr Thr Arg Leu Thr Trp Leu His Glu Lys Ile Leu Gln

1 5 10 15

Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val

20 25 30

His Gly Phe Arg Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly

35 40 45

Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr

50 55 60

Ala Glu Glu Ser Tyr Gln Glu Gly Lys Tyr Ala Ser Ile Ile Leu Phe

65 70 75 80

Ala Leu Gln Asp Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Cys Thr

85 90 95

Pro Glu Thr Leu Phe Cys Cys Asp Val Thr Lys Tyr Asn Ser Pro Thr

100 105 110

Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys

115	120	125
Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln		
130	135	140
Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile		
145	150	155
Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr		
165	170	175
Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu		
180	185	190
Gly Pro Ile Gly Ala Pro Lys Ser Ser Phe Phe Asn Ser Val Arg Ser		
195	200	205
Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr		
210	215	220
Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys		
225	230	235
Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser		
245	250	255
Glu Lys Glu Gly Gly Leu Cys Arg Asp Asp Ile Phe Tyr Ile Leu Asn		
260	265	270

Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys

275

280

285

Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile

290

295

300

His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Gln Tyr Phe Ser

305

310

315

320

Ser Gln Met Ile Val Lys Ile Lys Arg Ile Gln Arg Glu Leu Val Asn

325

330

335

Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp

340

345

350

Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Glu Pro Val

355

360

365

Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser

370

375

380

Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro

385

390

395

400

Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala

405

410

415

Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu

420

425

430

Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys

435

440